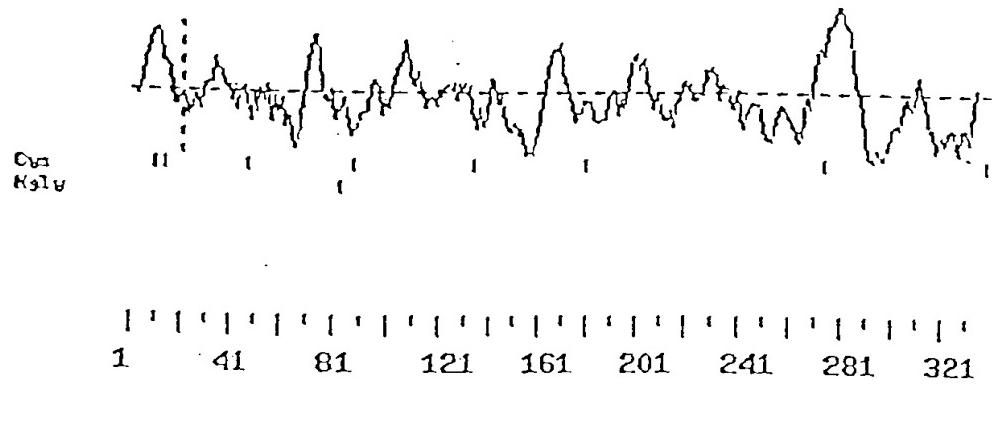


	H	S	P	S	P	T	A	L	F	C	L	
GGAGTCGACCCACCGCTCCGAGGGCTGAGGAACC	ATG	TCT	CCA	TCC	CCG	ACC	GCC	CTC	TTC	TGT	CTT	11
GGG CTG TGT CTG GGG CGT GTG CCA GCG CAG AGT GGA CCG CTC CCC AAG CCC TCC CTC CAG												68
G L C L G R V P A Q S G P L P K P S L Q												31
GCT CTG CCC ACC TCC CTG GTG CCC CTG GAG AAG CCA GTG ACC CTC CGG TGC CAG GGA CCT												128
A L P S S L V P L E K P V T L R C Q G P												51
GCT CTG CCC ACC TCC CTG GTG CCC CTG GAG AAG CCA GTG ACC CTC CGG TGC CAG GGA CCT												188
P G V D L Y R L E K L S S S R Y Q D Q A												71
CCG GGC GTG GAC CTG TAC CGC CTG GAG AAG CTG AGT TCC AGC AGG TAC CAG GAT CAG GCA												246
V L F I P A M K R S L A G R Y R C S Y Q												91
GTC CTC TTC ATC CCG GCC ATG AAG AGA AGT CTG GCT GGA CGC TAC CGG TGC TCC TAC CAG												308
N G S L W S L P S D Q L E L V A T G V F												111
AAC GGA AGC CTC TGG TCC CTG CCC AGC GAC CAG CTG GAG CTC GTT GCC ACG GGA GTT TTT												368
A K P S L S A Q P G P A V S S G G D V T												131
GCC AAA CCC TCG CTC TCA GCC CAG CCC GGC CCG GCG GTG TCG TCA GGA GGG GAC GTA ACC												428
L Q C Q T R Y G F D Q F A L Y K E G D P												151
CTA CAG TGT CAG ACT CGG TAT GGC TTT GAC CAA TTT GCT CTG TAC AAG GAA GGG GAC CCT												488
A P Y K N P E R W Y R A S F P I I T V T												171
GCG CCC TAC AAG AAT CCC GAG AGA TGG TAC CGG GCT AGT TTC CCC ATC ATC ACG GTG ACC												548
A A H S G T Y R C Y S F S S R D P Y L W												191
GCC CAC AGC GGA ACC TAC CGA TGC TAC AGC TTC TCC AGC AGG GAC CCA TAC CTG TGG												608
S A P S D P L E L V V T G T S V T P S R												211
TCG GCC CCC AGC GAC CCC CTG GAG CTT GTG GTC ACA GGA ACC TCT GTG ACC CCC AGC CGG												668
L P T E P P S S V A E F S E A T A E L T												231
TTA CCA ACA GAA CCA CCT TCC TCG GTA GCA GAA TTC TCA GAA GCC ACC GCT GAA CTG ACC												728
V S F T N K V F T T E T S R S I T T S P												251
GTC TCA TTC ACA AAC AAA CTC TTC ACA ACT GAG ACT TCT AGG AGT ATC ACC ACC AGT CCA												788
K E S D S P A G P A R Q Y Y T K G N L V												271
AAG GAG TCA GAC TCT CCA GCT GGT CCT GCC CGC CAG TAC TAC ACC AAG GGC AAC CTG GTC												848
R I C L G A V I L I I L A G F L A E D W												291
CGG ATA TGC CTC CGG GCT GTG ATC CTA ATA ATC CTG CGG GGG TTT CTG GCA GAG GAC TGG												908
H S R R K R L R H R G R A V Q R P L P P												311
CAC AGC CGG AGG AAG CGC CTG CGG CAC AGG GGC AGG GCT GTG CAG AGG CCG CTT CCG CCC												968
L P P L P Q T R K S H G G Q D G G R Q D												331
CTG CGG CCC CTC CGG CAG ACC CGG AAA TCA CAC GGG GGT CAG GAT GGA GGC CGA CAG GAT												1028
V H S R G L C S *												340
GTT CAC AGC CGC GGG TTA TGT TCA TGA												1055

FIGURE 1

CCGCTGAACCCAGGCACGGTGTATCAAGGGAGGGATCATGGCATGGAGGCAGTCAAAGACTGGCGTGTGGAGC 1134
CGTGGAAAGCAGGAGGGCAGAGGGCTACAGCTGTGAAACGAGGCCATGCTGCCCTCCCTGGTGTTCATCAGGGAGCCG 1213
TTGGGCCAGTGCTGCTGTGCTGCTCTGCTGAGGGCACCCCTCCATTGGGATGGAAGGAATCTGTGGAGAC 1292
CCCACCTCCCTCCCTGCACACTGTGGATGACATGGTACCCGGCTGGACCACATACTGGCCCTTTCTCAACCTCTCT 1371
AATATGGGCTCCAGACGGATCTAAGGTTCCAGCTCTAGGGTTGACTCTGTTCCATCTCTGTGCAAAATCTCTCT 1450
GTGCTCCCTTGGCCCTCTGTCTCTGCTGGTTTCCAGAAAATCTCACCCCTCACTCCATCTCCACTGCGGTC 1529
TAACAAATCTCCTTCTGCTCTCAGAACGGGTCTGCAGGCAGTTGGGTATGTCATTCAATTCTCTAGTGTAAAAT 1608
AGCACGTTGCCCTCCCTCACATTAGAAAAACAGATCAGCCTGTGCAACATGGTGAACCTCATCTCTACCAACAA 1687
AACAAAAAAACACAAAAATTAGCCAGGTGGTGGTGGCATCCCTATACTCCAGCAACTGGGGGGCTGAGGTGGAGA 1766
ATGGCTTGAGCCTGGGAGGCAGAGGTTGCACTGAGCTGAGATCACACCACTGCACTCTAGCTGGGTGACGAAGCTGA 1845
CCTTGCTCAAAAAATACAGGGATGAATATGTCAATTACCCGTATTGATCATGACACGTTGATAACATGTACTGCAAT 1924
ATTGCTGTCCACCCATAAAATATGTACAATTATGTATACTTTAAAAATCATAAAAATAAGATAATGAAAAAAAAA 2003
AAAAAAAAAAAGGGCGGGCGCTAGACTAGTCTAGAGAACAA 2047

FIGURE 1 cont.



MSPSPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPPGVLDYRLE
KLSSSRYQDQAVLFIPAMKRSLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQP
GPAVSSGGDVTLQCQTRYGFDQFALYKEGDPAPYKNPERWYRASFPIITVTAHSGTYRC
YSFSSRDPYLWSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSSEATAELTVSFTNKVFT
TETSRISITTSPKESDSPAGPARQYYTKGNLVRICLGAVILIIILAGFLAEDWHSRRKRLRH
RGRAVQRPLPPLPQTRKSHGGQDGGRQDVHSRGLCS

FIGURE 2

ALIGN calculates a global alignment of two sequences
version 2.0uPlease cite: Myers and Miller, CABIOS (1989)
> U91928 ORF 1893 aa vs.
> ht268 ORF 1017 aa
scoring matrix: paml20.mat, gap penalties: -12/-4
37.7% identity; Global alignment score: -8

10	20	30	40	50	60	70
inputs ATGACGCCGCCCTCACAGCCTGCTGCCTGGCTGAGTCTGGCCCCAGGACCCGGCGTGCAGGCAG						
::: ::						
ATGTCTCCATCCCCGACCGCCTTCTGTCTTGGCTGTCTGGCCG-TGTGCCAGC-GCAGAGTG						
10	20	30	40	50	60	
80	90	100	110	120	130	
inputs CGCCCTTCCCCAAACCCACCCCTGGGCTGAGCCAGGCTCTGTGAT-CAGCTGGGGAGCCCCGTGACCA						
::: ::						
GACCGCTCCCAAGCCCTCCCTCCAGGCTCTGCCAGCTCCCTGGTGCCTGGAGAAGCCA-GTGACCC						
70	80	90	100	110	120	130
140	150	160	170	180	190	200
inputs TCTGGTGTCAAGGGAGCCTGGAGGCCAGGAGTACCGACTGGATAAAGAGGGAAAGCCCAGAGCCCCTTGGA						
::: ::						
TCGGGTGCCAGGG--ACCT-----CCGGCGTG--GACCTGTA-----CCGCCTGGAG----AAG						
140	150	160	170	180		
210	220	230	240	250	260	270
inputs CAGAAAATAACCCACTGGAACCCAGAACAGGCCAGATTCTCCATCCCATGACACAGCACCACATGGG						
::: ::						
CTGAGTT--CCAGCAGGTACC-AGGATCA-GGCAGTCCCTTCATCCGCCATGAAGAGAAGTCTGGCT						
190	200	210	220	230	240	
280	290	300	310	320	330	340
inputs GGGAGATACCGCTGCCACTATTACAGCTGGCAG--GCTGGTCAGAGGCCAGGACCCCTGGAGCTGGT						
::: ::						
GGACGCTACCGCTGCTCTAC--CAGAACGGAGCCTGGTCCCTGCCAGCGACCAGCTGGAGCTCGT						
250	260	270	280	290	300	310
350	360	370	380	390	400	410
inputs GATGACAGGATTCTACAACAAACCCACCCCTCTCACGCCCTGCCAGCCCTGTGGTGGCCTCAGGGGGAAAT						
::: ::						
TGCCACGGGAGTTTGCCAAACCCCTCGCTCTCACGCCAGGCCGGCCGGCGGTGTCGTCAAGGAGGGAC						
320	330	340	350	360	370	380
420	430	440	450	460	470	480
inputs ATGACCCCTCCGATGTGGCTCACAGAACGGATATCACCATTTGTTCTGTGATGAAGGAAGGAGAACACCAGC						
::: ::						
GTAACCCCTACAGTGTCAAGACTCGGTATGGCTTGACCAATTGCTCTGTACAAGGAAGG-----						
390	400	410	420	430	440	
490	500	510	520	530	540	550
inputs TCCCCCGGACCCCTGGACTCACAGCAGCTCCACAGTGGGGGTTCCAGGCCCTGTGGCCCCGT						
::: ::						

FIGURE 3

GGACCCCTG-----C---GCCCTA-----CAA
 450 460
 560 570 580 590 600 610 620
 inputs GAACCCAGCCACAGGTGGAGGTCACATGCTATTACTATTATGAACACCCCCCAGGTGTGGTCCCAC
 ::::: ::::: ::::: ::::: ::::: ::::: :::
 GAATCCCGA-----GAGATGGTAC-CGGGCTAGT- ---TT--- CCCCAT-----CAT
 470 480 490 500
 630 640 650 660 670 680 690
 inputs CCCAGTGACCCCCCTGGAGATTCTGCCCTCAGGCGTGTCTAGGAAGCCCTCCCTCTGACCCCTGCAGGGCC
 ::::: ::::: ::::: :::
 CACGGTGACCGCC-----GCCACAG-
 510 520
 700 710 720 730 740 750 760
 inputs CTGTCCTGGCCCCCTGGGCAGAGCCCTGACCCCTCCAGTGTGGCTCTGATGTCGGCTACGACAGATTGTTCT
 ::::: ::::: ::::: :::
 CGGAACCTA-----CCGATG-----CTACAGC-----TTCT
 530 540 550
 770 780 790 800 810 820 830
 inputs GTATAAGGAGGGGGAACGTGACTTCCAGGCCCCCTGGCCAGCAGCCCCAGGCTGGCTCTCCAGGCC
 ::::: :::::
 CCAGCAG-----
 840 850 860 870 880 890 900
 inputs AACTTCACCCCTGGGCCCTGTGAGCCCCCTCCCACGGGGCCAGTACAGGTGCTATGGTGACACAAACCTCT
 ::::: :::::
 GGACCCA-----TACCT--
 560
 910 920 930 940 950 960 970
 inputs CCTCCGAGTGGTCGGCCCCCAGCGACCCCTGACATCCCTGATGGCAGGACAGATCTATGACACCGTCTC
 ::::: ::::: ::::: :::
 GTGGTCGGCCCCCAGCGACCCCTCGA-----GCT-----TGTG-----
 570 580 590 600
 980 990 1000 1010 1020 1030 1040
 inputs CCTGTCAGCACAGCCGGGGCCCACAGTGGCCTCAGGAGAGAACGTGACCCCTGCTGTCAGTCATGGTGG
 ::::: ::::: ::::: :::
 GTCA-----CAGGAACCTCTGTGACC-----CCCAGC-----CGGT-----
 610 620 630
 1050 1060 1070 1080 1090 1100 1110
 inputs CAGTTTGACACTTCCCTCTGACCAAAGAAGGGCAGCCCATCCCCACTGCGTCTGAGATCAATGTACG
 ::::: ::::: :::
 TACCAACAGAAC-----CA-----CCTTCC-----TCG-----
 640 650
 1120 1130 1140 1150 1160 1170 1180

FIGURE 3 cont.

inputs GAGCTCATAAGTACCAAGGCTGAATTCCCAGTCCTGTGACCTCAGCCACGGGGACCTACAGGTG
 ::
 GTA-----GCAGAATTCTC-----AGAACCCAC-----CGCTGA-----ACTG---A
 660 670 680 690
 1190 1200 1210 1220 1230 1240 1250
 inputs CTACGGCTCATACAGCTCCACCCCCACCTGCTGTCTTCCCCAGTGAGCCCCCTGGAACCTCATGGCTCTA
 :
 C---GCTCTCATCTA---CAAACT---AAAGTCTT---CACAA---CTGAGACT---TCT---
 700 710 720 730
 1260 1270 1280 1290 1300 1310 1320
 inputs GGACACTCTGGAGGCTCCAGCCTCCCACCCACAGGGCCGCCCTCACCTGGCTGGGAAGATAACCTGG
 . :
 -----AGGAGTATC--ACCACCAAGTCCAAAGGA--GTCAGACTCTCCAG--CTGG-----
 740 750 760 770
 1330 1340 1350 1360 1370 1380 1390
 inputs AGCTTTGATTGGGGTCTCGTGGCCITCGTCTGCTGCTCTCCCTCTCTCTCTCTCCGAGG
 :
 TCGTGC-----CCGCCAGTA---CTACACCAAGG
 780 790 800
 1400 1410 1420 1430 1440 1450 1460
 inputs TCAGCGTCACAGCAACACAGGACATCTGACCAAGAAAGACTGATTCCAGCGCTCTGCAGGGCTGCG
 ::
 GCAAC-----CTGGTC-----CGGATAT---GCCTC---GGGGCTG--
 810 820 830
 1470 1480 1490 1500 1510 1520 1530
 inputs GAGACAGAGCCCAAGGACAGGGCCTGCTGAGGAGGTCCAGCCCAGCTGCTGACCTCCAGGAAGAAAACC
 . :
 -----TGATCCTAATAA----TCCTG--GGGGGTTCTG-----GCAGA-GGACTGG-----C
 840 850 860 870
 1540 1550 1560 1570 1580 1590 1600
 inputs TCTATGCTGCCGTGAAGGACACACAGTCTGAGG-ACAGGGTGGAGCTGGACAGT-CAGAGCCCACACGAT
 . :
 AC----AGCGG--GAGGAAGCGC--CTGGGGCACAGGG---GCAGGGCTGTGCAGAGGGCGCT---
 880 890 900 910 920
 1610 1620 1630 1640 1650 1660 1670
 inputs GAAGACCCCCAGGCAGTGACGTATGCCCGGTGAAACACTCCAGTCCTAGGAGACAATGGCTCTCCTC
 . :
 ---TCC-----GCCCTG-----CCGC---C
 930 940
 1680 1690 1700 1710 1720 1730 1740
 inputs CCTCCCTCACTGTCTGGGAATTCTGGACACAAAGGACAGACAGGTGGAAGAGGGACAGGCAGATGGACAC
 . :
 CCTCC-OGCAGAC-----CGGAAATCA-----CA-CGGG-----GGTCAGG---ATGGA---
 950 960 970 980

FIGURE 3 cont.

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  1750      1760      1770      1780      1790      1800      1810
inputs TGAGGCTGCTGCATCTGAACGCCCTCCAGGATGTGACCTACGCCAGCTGCACAGCTTGACCCCTTACACCG
      ::::     :::::     :::::::     :::::::     :::::::     :::::
      ---GGC---CGAC-----AGGATGTT-----CACAGC-----CGA-
      990                  1000

  1820      1830      1840      1850      1860      1870      1880
inputs AAGGCAACTGAGCCTCCTCCATCCCAGGAAGGGAACCTCCAGCTGAGCCCAGCATCTACGCCACTCTGG
      :::::::   :::::
      -----CGGGTTATG-----TTCA-----
      1010

  1890
inputs CCATCCAC

```

FIGURE 3 cont.

ALIGN calculates a global alignment of two sequences
version 2.0. Please cite: Myers and Miller, CABIOS (1989)
> hT268 a.a. 339 aa vs.
> GenPept U91928 - Human clone HL9 monocyte inhib 631 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
23.0% identity; Global alignment score: -642

	10	20	30	40	50	60		
inputs	MSPSPTAFLPCLGLCIG-RVPAQSGPLPKPSLQALPSSIVPLEKPVTLRQCGPPHUNTDYRLDKLSS-							
 : .							
	MTPALTAI-LCLGLSLGPRTRVQAGPPPKPTIWAEPGSVISWGSPVTIWCQGSLEAQSBYRIDLKEGSPEPLD	10	20	30	40	50	60	70
	70	80	90	100	110	120	130	
inputs	RYQ-----DQAVLFIPAMKRSLAGRYRCSYQNGLSWSLPSDQLELVATGVFAFPSLSAQPGPAVSSGGDV							
	: : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : .							
	RNNPLEPKNYARFSIPSMTEHHAGRYRCHYYSSAGWSEPSDPLELVMTCFYNTPTSLALPSPVVASGGNM	80	90	100	110	120	130	140
inputs	TIQCQT-----							
	:							
	TLRCGSQKGYHHFVLMKEGEHQLPRTLDSQQLHSGGFQALFPVGVPVNPShRWFTCYYYYYMMNTPQVWSHP	150	160	170	180	190	200	210
	140	150						
inputs	-----GFDQFALYKEGOP-----							
	: : . .							
	SDPLEILPSGVSRRPSLLTLQGPVLAPGQSLTLQCGSDVGYDRFVLYKEGERDFLQRPGQQPQAGLSQAN	220	230	240	250	260	270	280
	160							
inputs	-----APYK-----NP-----ERW-----							
	: : . .							
	FTLGPVSPSHGQYRCYGAHNLSSSEWSAPSPLNILMAGQIYDTVSLSAQPGPTVASGENVTLLCQSQWHQ	290	300	310	320	330	340	350
	170	180	190	200				
inputs	-----YRASFPIITVTAHSGCTYRCYSFSSRDPYLWSAPS DPLELVVTG							
	: : . . : . . : . . : . . : . . : . . : . . : . . : . . : . . : . . : . .							
	FDTFLLTKEAAHPPLRLRSMYGAHKYQAEPHSPVTSAAHGTYRCYGSYSSNPHLSPSEPLELMVSG	360	370	380	390	400	410	420
	210	220	230	240	250	260		
inputs	TSVTPSRLPTEPPSS--VAEFSEATAELTVSFTNKVF-----TTETSRISITSPKESD--SPAGPA-							
	: : . . : . . : . . : . . : . . : . . : . . : . . : . . : . . : . . : . .							
	HSGGSSLPPTPGPPSTPGLGRYLEVLIGVSVAFVLLLFLRLRRQRHSKHRTSDQRKTFDQRPAAGAE	430	440	450	460	470	480	490
	270	280	290					
inputs	RQYYTKGNLVRICLGAVID---IILAGFLAEDW-----HSRRKR-----							
	: : . . : . . : . . : . . : . . : . . : . . : . . : . . : . . : . .							

FIGURE 4

TEPKDRGLLRRSSPAADVQEEENLYAAVKDTQSEDRVELDSQSPHDEDPQAVTYAPVKHSSPRREMASPPS
500 510 520 530 540 550 560

300 310 320 330
inputs -----LRHRGRAVQ--RPL-----PPLPPLPQTRK-----SHGGQDGGRQDVHSRGLC
: . : .
SLSGEFLDTKDRQVEEDRQMDTHEAAASEASQDVTYAQLHSLTLRRKATEPPPSQEGERPAEPSIYATLAI
570 580 590 600 610 620 630

inputs S

H

FIGURE 4 cont.

Alignments of top-scoring domains:

ig: domain 1 of 2, from 41 to 90: score 4.1, E = 6.1

*->GesvtLtcsvsgfgppgvsvtWYfkngk.lgpsllgysysrlesgek
hT268 41 EKPVTLRCQGP-----PGVDLY-RLEK1SSS-----RYQDQ-- 70
enlsegrfsissltLtissvekeDsGtYtCvv<-*
hT268 71 -----AVLFIPAMKRSLAGRYRCSY 90

FIGURE 5A

```

ig: domain 2 of 2, from 127 to 182: score 19.1, E = 0.1
      *->GesvtLtCsvsgfgppgvsvtWfyfkngk.lgpsllgysysrlesgek
      G++vtL+C++ + ++ Y k+g++ + y+++
ht268 127      GGDVTLQCQTR---YGFDFQFALY-KEGDPAP-----YKNPERWYR-- 167

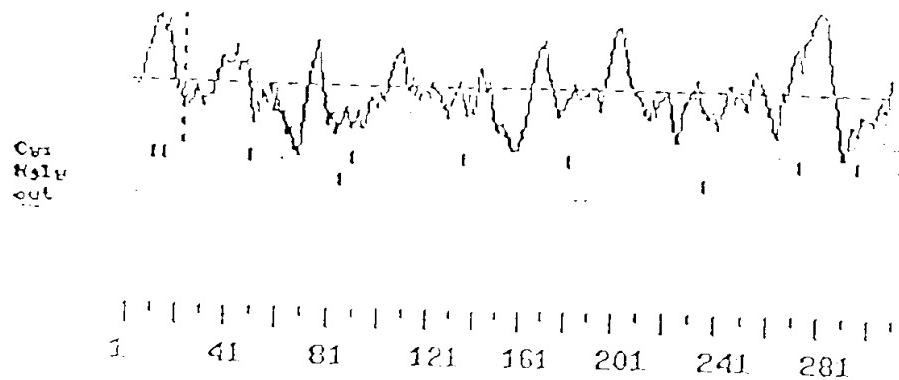
      anlsegrfsissltLtissvekeDsGtYtCvv<-*
      +++i++v++ sGtY+C
ht268 163      -----ASFPIITVTAAHSGTYRCYS 182

```

FIGURE 5B

	M	S	P	A	4
GAGTCGACCCACCGCTCCGCTCCCTGCTGGCCACATAGCTCAGGACTGGGTGGCAGAACCAATG TCT CCA GGC					74
S P T F F C I G L C V L Q V I Q T Q S G					24
TCA CCC ACT TTC TTC TGT ATT GGG CTG TGT GTA CTC CAA GTG ATC CAA ACA CAG AGT GGC					134
P L P E P P S L Q A Q P S S L V P L G Q S					44
CCA CTC CCC AAA CCT TCC CTC CAG G T CAG CTC ATT TCC CTC GTA CTC CTC CTC CTC CTC CTC					134
V I L R C Q G P I D V D I Y L L H E K D E					64
GTT ATT CTC AGG TCC CAG GGA CCT CCA GAT GTG GAT TTA TAT CGG CTC GAG AAA CGT AAG					254
P E K Y E D Q D F L F I P T M E E S N I					84
CCG GAG AAG TAT GAA GAT CAA GAC TTT CTC TTC ATT CCA ACC ATG GAA AGA AGT AAT GCT					314
G R Y R C S Y Q N G S H W S L P S D Q L					104
GGA CGG TAT CGA TGC TCT TAT CAG ATT GGG AGT CAC TGG TCT CTC CCA ACT GAC CAG CTC					374
E L I A T G V Y A R P S L S A H P S S A					124
GAG CTA ATT GCT ACA GGT GTG GAT GTC CCT AAA CGT TCA CTC TCA GTC CAT CGG AGT TCA GTC					434
V I Q G R D V T I E C C S I Y S P D E F					144
GTC CCT CCA GGC AGG GAT GTG ACT CTC AAG TCC CTC CTC AGC CCA TAC AGT TTT GAT GAA TTC					494
V L Y K E G D T G P Y E R P E H W Y R A					164
GTT CTA TAC AAA GAA GGG GAT ACT GGG CCT TAT AAG AGA CCT CAG AAA TGG TAC CGG GCG					554
N F P I I T V T A A H S G T Y R C Y S F					184
AAT TTC CCC ATC ATC ACA GTG ACT GCT GCT CAC AGT GGG ACG TAC CGG TGT TAC AGC TTC					614
S S S S P Y L W S A P S D P L V L V V T					204
TCC AGG TCA TCT CCA TAC CTG TGG TCA GCC CCG AGT GAC CCT CTA GTG CTT GIG GTT ACT					674
G L S A T P S Q V P T E E S F P V T E S					224
GGA CTC TCT GCC ACT CCC AGC CAG GTC CCC ACG GAA TCA TTT CCT GTG ACA GAA TCC					734
S R E P S I L P T N K I S T T F K P M N					244
TCC AGG AGA CCT TCC ATC TTA CCC ACA AAC AAA ATA TCT ACA ACT GAA AAG CCT ATG AAT					794
I T A S P E G L S P P I G F A H Q H Y A					264
ATC ACT GCC TCT CCA GAG GGG CTG AGC CCT CCA ATT GGT TTT GCT CAT CAG CAC TAT GCC					854
K G N L V R I C L G A T I I I I L L G L					284
AGG GGG AAT CTG GTC CGG ATA TCC CTT GGT GCC AGC ATT ATA ATA ATT TTG TTG GGG CTT					914
L A E D W H S R K K C L Q H R M R A L Q					304
CTA GCA GAG GAT TGG CAC AGT CGG AAG AAA TGC CTG CAA CAC AGG ATG AGA GCT TTG CAA					974
R P L P P' L P L A *					314
AGG CCA CTA CCA CCC CTC CCA CTG GCC TAG					1004
AAATAACTTGGCTTTCAGCAGAGGGATTGACCAGACATCCATGCCACAAACCATGGACATCACCACAGGCCACAGACAT					1083
GGACATACTCAAGAGTGGGGAGGTTATATAAAGGTTATGAGTGTGGAGAATAATGCAAGAGCCACAAAGGTGAAAAAAA					1162

FIGURE 6



MSPASPTFFCIGLCVLQVIQTQSGPLPKPSLQAQPSSLVPLGQSVILRCQGPPDVDLYRL
EKLKPEKYEDQDFLFIPTMERSNAGRYRCSYQNGSHWSLPSDQLELLIATGVYAKPSSL
PSSAVPQGRDVTLKCQSPYSFDEFVLYKEGDTGPYKRPEKWYRANFPIITVTAHSCTYR
CYSFSSSSPYLWSAPSDPLVLTGSLATPSQVPTTEESFPVTTESSRRPSILPTNKISTTE
KPMNITASPEGLSPIGFAHQHYAKGNLVRICLGATIIIIILLGLLAEDWHSRKKCLQHRM
RALQRPLPPLPLA

FIGURE 7

FIGURE 8

FIGURE 8 cont.

```

inputs GCTCATAAGTACCAGGCTGAATTCCCCATGAGTCCTGTGACCTCAGCCCACGCCGGGACCTACAGGTGCT
: : . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . .
G--AAATGGTACCGGGCAATTCCCCATCATCACACTGACTGCTGCTCACAGTGGGACGTACCGGTGTT
480      490      500      510      520      530      540

1190      1200      1210      1220      1230      1240      1250
inputs ACGGCTCATACAGCTCAACCCCCACCTGGCTCTTCCCCAGTGAGGCCGTGGAAACTCATGGTCTCAGG
: . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . .
ACAGCTCTCCAGCTCATCTCATACTTGTCAGGCCGGAGTGACCCCTGTTACTGCTTGTTACTGG
550      560      570      580      590      600      610

1260      1270      1280      1290      1300      1310      1320
inputs ACACCTGGAGGCTCCAGCCTCCCACCCACAGGGCCGCCCTCCACACCTGGCTGGGAAGATAACCTGGAG
: . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . .
ACTCTCTG----CCA--CTCCAGCC--AGGT--ACCCAC-----GGA-AGAATCATTCTCG---
620      630      640      650      660

1330      1340      1350      1360      1370      1380      1390
inputs GTTTGATGGGAACTCGGGGGCTCTGCTGCTCTTCTCTCTCTCTCTCTCTCCGACGTC
: . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . .
---TGA---CAGATCTT---GAGAGACUTTCCA---TCATAC---CCACAAACAAA
670      680      690      700

1400      1410      1420      1430      1440      1450      1460
inputs AGCGTCACAGCAAACACAGGACATCTGACCAGAGAAAGACTGATTTCCAGCGTCTGCAGGGGCTGGGA
: . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . .
A---TATCTACAA---CTGAA---AAGCCTATGAATATC--ACTGCCT-C-TCCAG-AGGGGCTG---
710      720      730      740      750

1470      1480      1490      1500      1510      1520      1530
inputs GACAGAGCCCCAAGGACAGGGGCCTGCTGAGGAGGTCCAGCCCAGCTGCTGACCTCAGGAAGAAAACCTC
: . . . . . . . . . . . . . . . . . . . . . . . . . . . .
---AGCCCT---CC---AATTGGTTTGCTCATCAGCA---C
760      770      780

1540      1550      1560      1570      1580      1590      1600
inputs TATGCTGCCGTGAAGGACACACAGTCTGAGGACAGGGTGGAGCTGGACAGTCAGAGCCCACACGATGAAG
: . . . . . . . . . . . . . . . . . . . . . . . . . . .
TATGC-----CAAGGGGAATCTGGTC-----CGGATATG
790      800      810

1610      1620      1630      1640      1650      1660      1670
inputs ACCCCCAGGCACTGACGTATGCCCGGTGAAACACTCCAGTCCTAGGAGAGAAATGGCCTCTCCCTCCCTC
: . . . . . . . . . . . . . . . . . . . . . . . . .
---CCTTGG-----TGCCACGAT-----TATAATAATTGT-----
820      830      840

1680      1690      1700      1710      1720      1730      1740
inputs CTCACTGTCTGGGAATTCTGGACACARAGGACAGACAGGTGGAAGAGGACAGGCAGATGGACACTGAG
: . . . . . . . . . . . . . . . . . . . . . . . . .
-----TGGGGCTT--CTAG---CAGAGGATTGGC-----ACAGTCGGAAGAA---AT
850      860      870      880

```

FIGURE 8 cont.

1750 1760 1770 1780 1790 1800 1810
inputs GCTGCTGCATCTGAAGCCTCCCAGGATGTGACCTACGCCAGCTGCACAGCTTACCCCTAGACGGAAAGG
:: :::::::
GC--CTGCAACA-----CAGGATGAGA-----GCTTTGC-----AAGG
890 900 910

1820 1830 1840 1850 1860 1870 1880
inputs CAACTGAGGCTCTCCATCCCAGGAAGGGAAACCTCCAGCTGAGGCCAGCATCTAGCCACTCTGGCCAT
:: :::::
CCACTA-----CCACC-----CCTCC-----CACTGGCC--
920 930

1890
inputs CCAC

FIGURE 8 cont.

FIGURE 9

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THEFDEGILRRGGPAADVQERNLYAAVKDTQSEDRVELDSQSPHDEDPQAVTYAIYAHSSPRREMASPPG
500 510 520 530 540 550 560

280 290 300 310
inputs CLGATIIIILLGLLAEDWH-----SRKKCLQHRMRALQRPL----PP-----LPL
...
SLSGEFLDTKDRQVEHDHQMDTEAAASEASQDVTYAQLHSLTLLRKATEPPPSQEGEPPAEPSEIYATLAI
570 580 590 600 610 620 630

Inputs: 7

H

FIGURE 9 cont.

Alignments of top-scoring domains:

1g: domain 1 of 2, from 42 to 91; score 10.2, E = 1.4
*->GesvtLtcsvsgfgppgvsvtWvfknk.lgpsllgysysrlesgek
MT268 42 G+sv L+C+ +v Y + k ++ +++e +
GQSVIIRCQGP-----PDVDLY-RLEK1KP-----EKYEDQ-- 71
anlsegrfaissltltissvekeDsGtYtCvv<- *
MT268 72 L i + e+ + + G Y+C -----DFIPIPTMERSNAGRYRCSY 91

FIGURE 10A

fig: domain 2 of 2, from 128 to 183; score 9.6, E = 1.6
*->GesvtLtcsvsgfgppgvsvtWyfkngk.lgpsllgysysrlesgek
MT268 128 G +vtL C++ + y k+g++ + y+r+e +
GRDVTLKCQSP---YSFDEFVLY-KEGDtGP-----YKRPEKW-Y 162
anlseggrfsissltLtissvekeDsGtYtCvv<-•
MT268 163 RA-----NFPIITVTAHSGTYRCYS 183

FIGURE 10B

ALIGN calculates a global alignment of two sequences

version 2.0. Please cite: Myers and Miller, CABIOS (1989).

> hT268 s.s.

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SCORING ENTRY: 500-130 = 370 points (134.4%)

Scoring matrix: pamp20.mat, gap penalties: -12/-6/-4; identity: Global Minima = 1051

88.4% identity; Global alignment score: 1011

10 20 30 40 50 60
 inputs HSPSPTALFCIGLCLIGRV-PAQSGPLPHPSLQLAPSSLVPLKEFVTLRCQQPPGVLDLYRLEKLSSRYQD
 ::::: .::: .::: .::: .::: .::: .::: .::: .::: .::: .::: .::: .::: .::: .::: .::: .:::
 HSPASPTFFCIGLCVLQVIQIAGSGPLPHPSLQAQPSSLVPLGQSVILRCQQPPDVLDLYRLEKLKPERYHD
 10 20 30 40 50 60 70

70 80 90 100 110 120 130
 inputs QAVLFIPAKRSLAGRYRCYSQNGSIWSDLPSDQLEIATGVFAFPSLSAQIYGPAAVESGCDVTIQCQTRYG
 :: ::::: :: ::::::::::::: ::::::::::::::: ::::::: ::::::: ::::::: : ::::::: . .
 QQFLFIPKTHRSNAGRYRCYSQNGSHWSLPSDQLEIATGVYAFPSLSAHPSSAVPQRDVTLKCQSPYS
 80 90 100 110 120 130 140

140 150 160 170 180 190 200
 inputs FDQFALYKEGDPAPYKQNPERWYRASFPIITVTAAGSGTYRCYSFSSRDPYLWSAPSDFLELVVTGTSVTP
 :::::::::::::::::::: :::::::::::::::::::: :::::::::::::::::::: :::::::::::::::::::: :::::::::::::::::::: :::::::::::: :::::::::::::
 FDEFVLYKEGDTGPYKRPEKWHYRANFPIITVTAAHSGTYRCYSFSSSPYLWSAPSDFPLVLVVTGLSATP
 150 160 170 180 190 200 210

210 220 230 240 250 260 270 ↓
 inputs SRLPTEPPSSVAEFSATAELTVSFTNKVTTETRSITTSRKESDSPAGPARQYYTKGNLVRICLGAVI
 : .
 SQVPTEESFPVTESSRRPSILP---TNKISTTEKPMNITASPEGLSPIGFAHQHYAKGNLVRICLGATI
 220 230 240 250 260 270

```

  280      290      300      310      320      330
inputs LIILAGFLAEDWHSRRKRLRHRGRAVQRPLPPLPPQTRKSHGGQDGGRQDVHSRGGLCS
       ::::::::::::::::::::: ::::::::::::::: :::
       IIIILGLIAEDWHSRKKCLQHMRALQRPLPPLP-LA-----
280      290      300      310

```

FIGURE 11

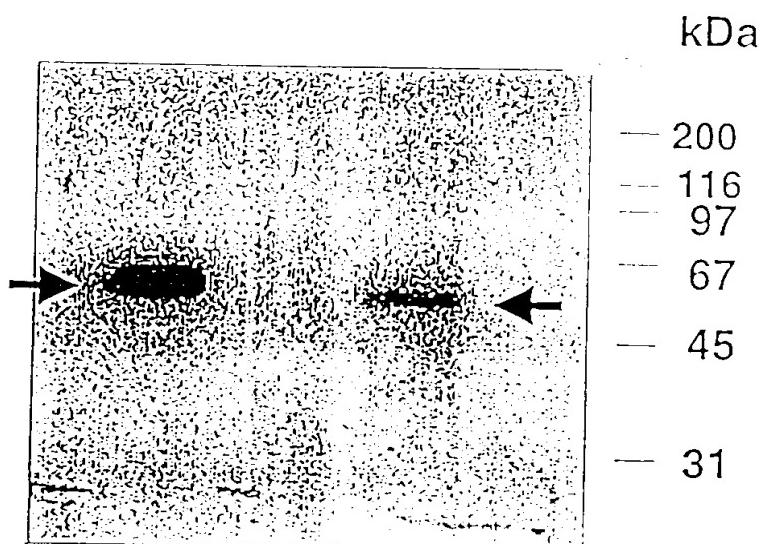


FIGURE 12

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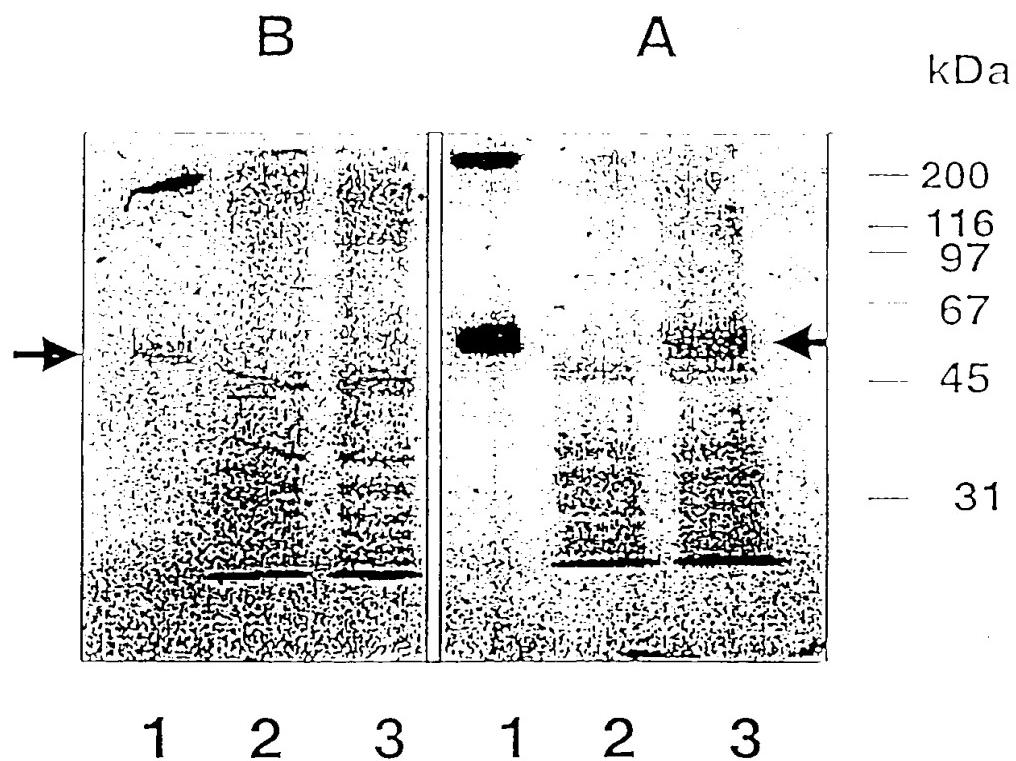
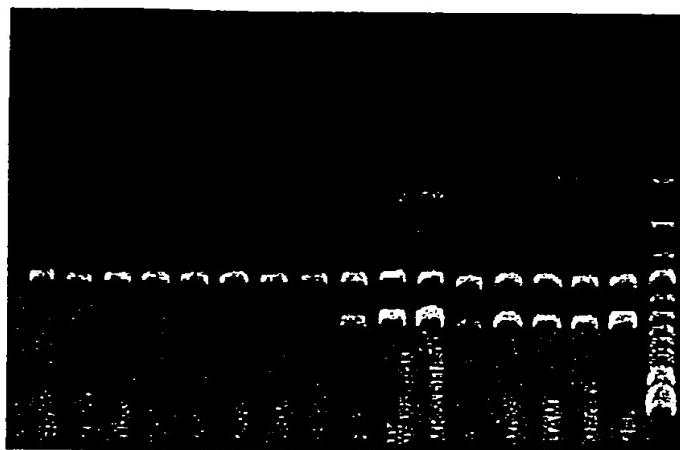


FIGURE 13



Sp LN Thy PBL BM FL

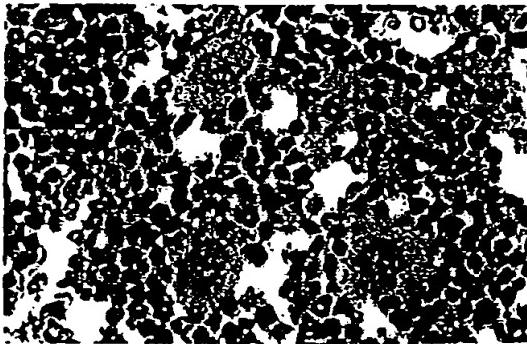
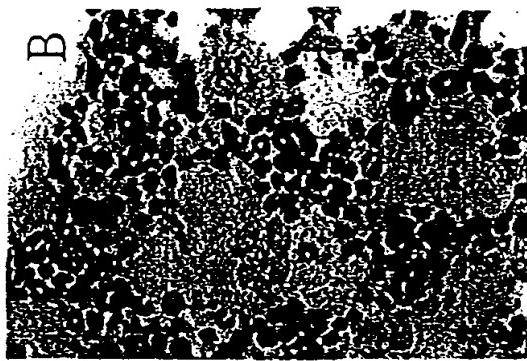
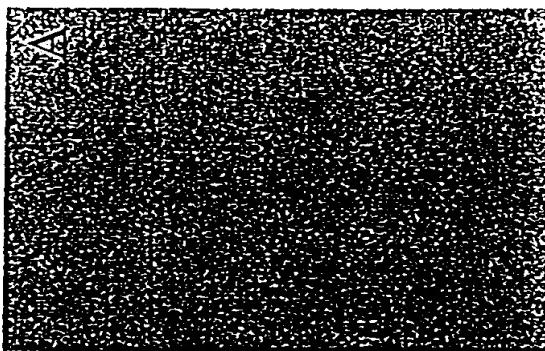
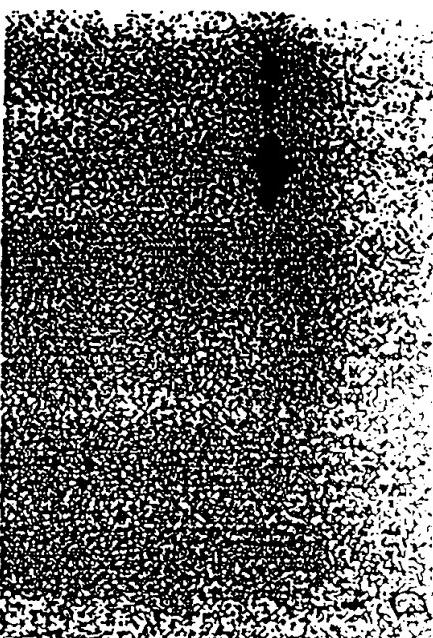
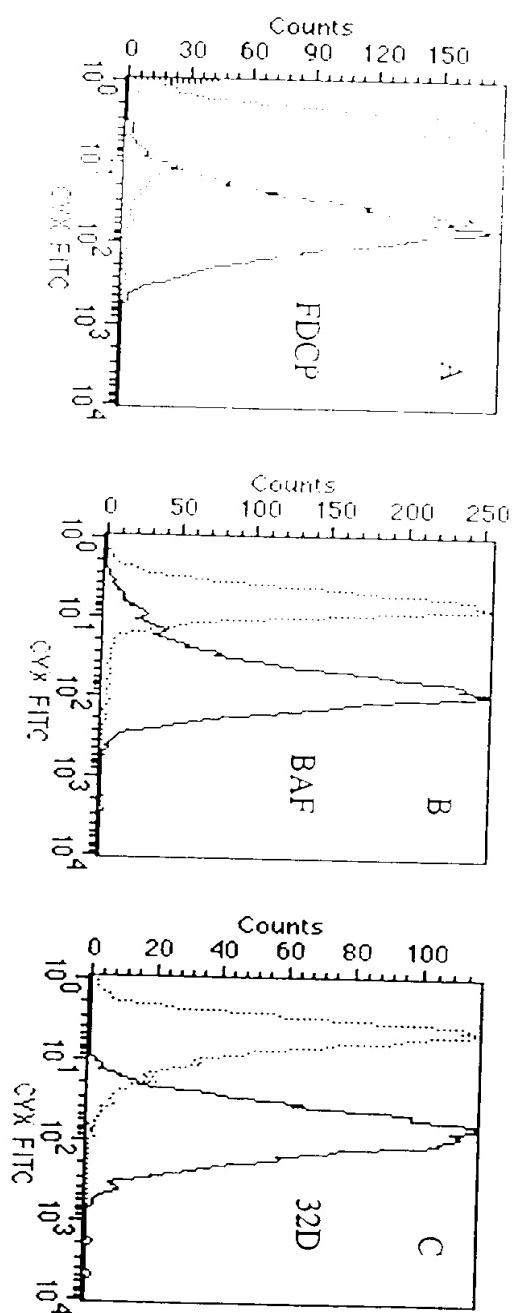


FIGURE 14

**FIGURE 15**

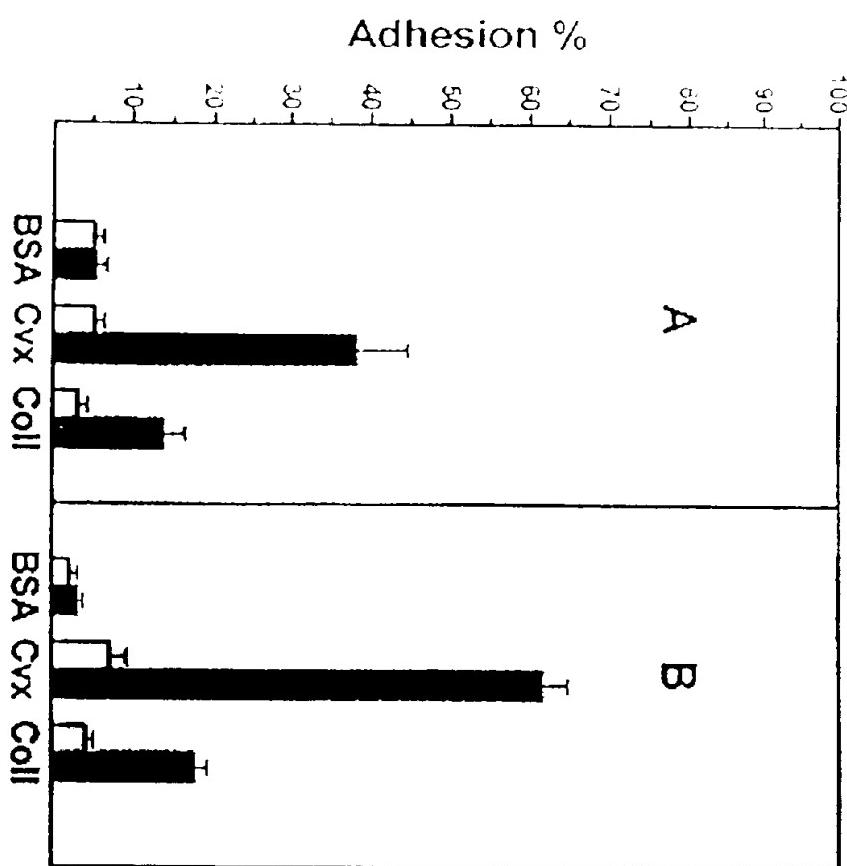


FIGURE 16

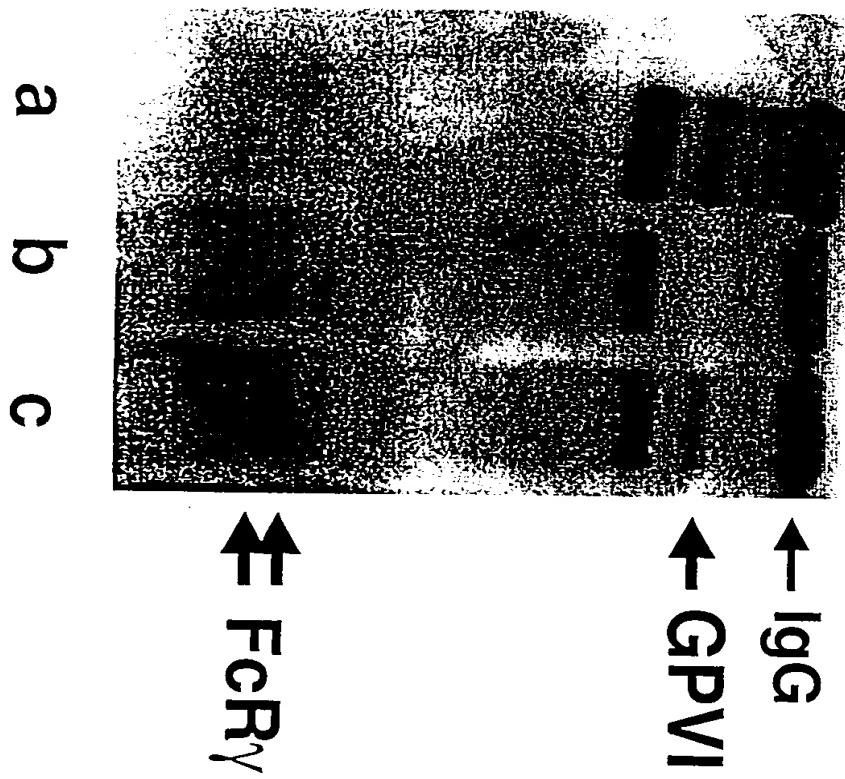
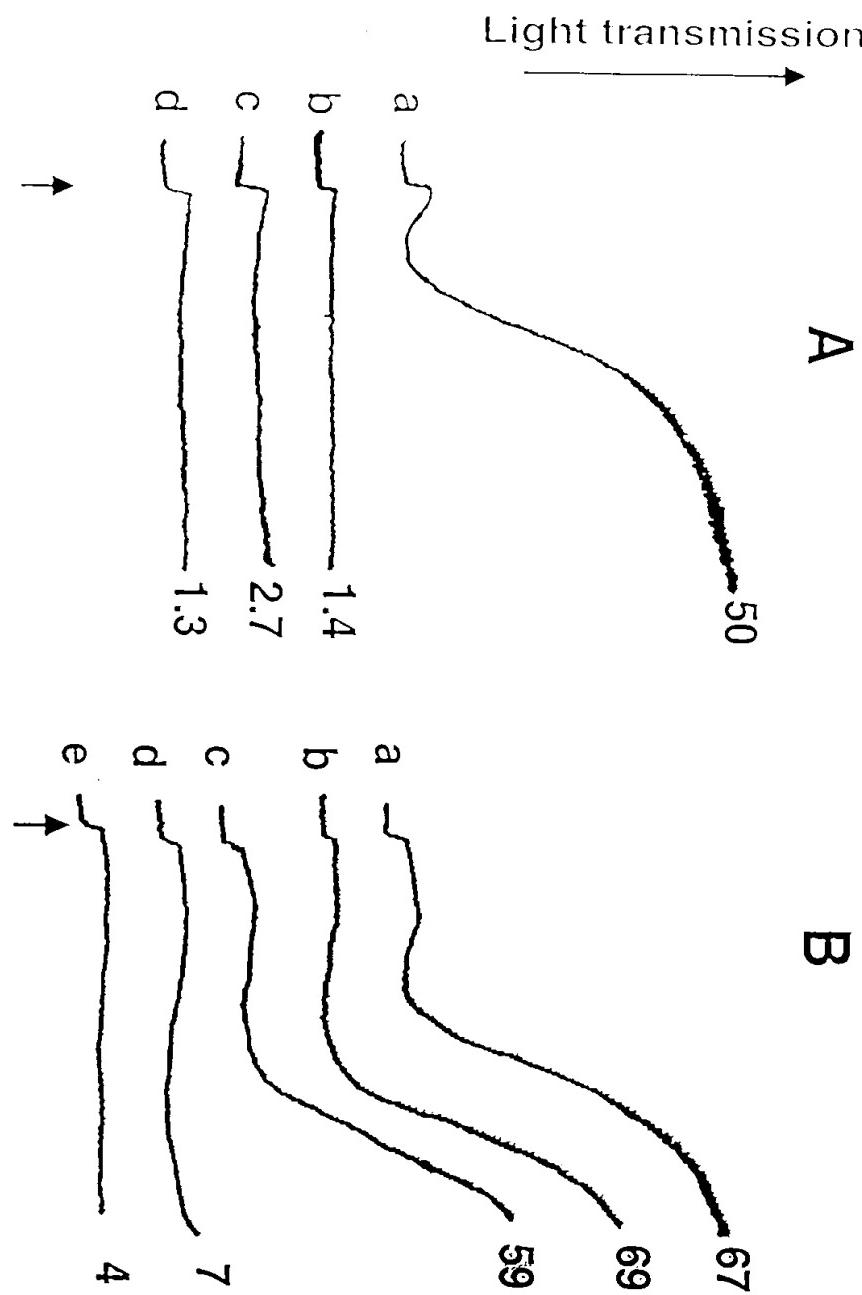


FIGURE 17

**FIGURE 18**

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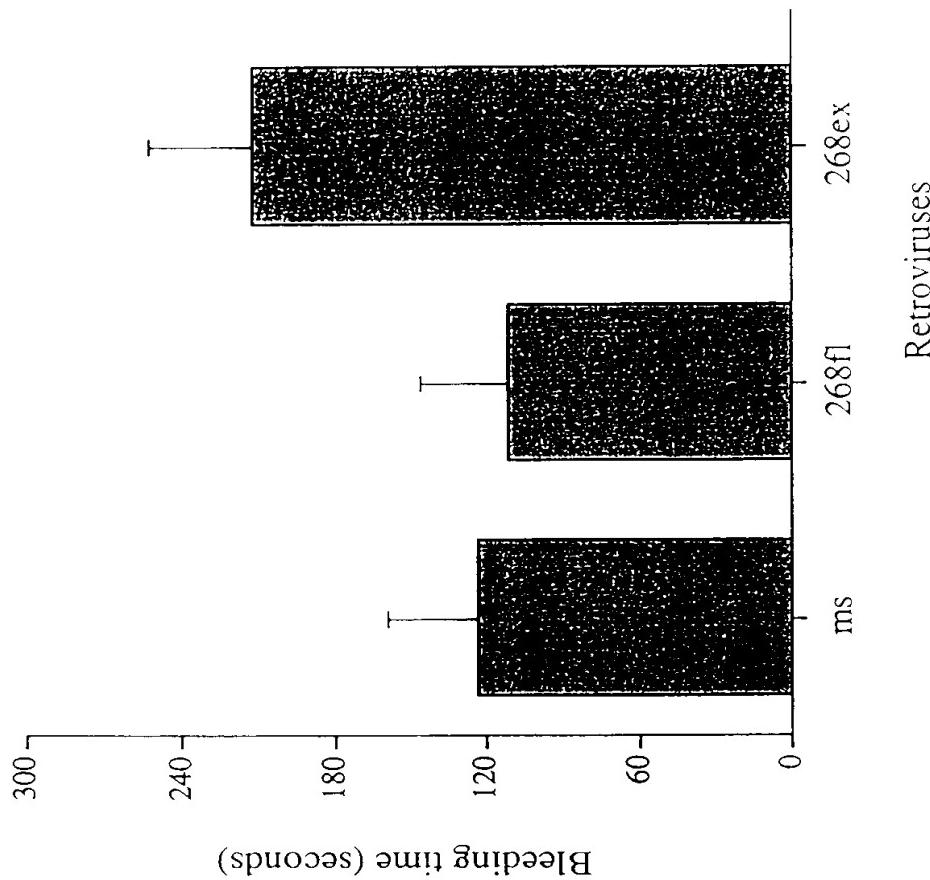


FIGURE 19